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13. ABSTRACT ***(Maximum 200 Words)***

Mammographic percent density is an established and important risk factor for breast cancer. We have previously shown that this risk factor has a considerable genetic component that may be the result of a single major gene. We are now working to localize this gene to an autosome. Simulation studies were performed on all study families (n=426). We identified 57 families in which multiple members have previously obtained mammograms. Primary efforts are to obtain DNA samples on these family members. To date, letters of invitation (consent forms) have been sent to more than half (n = 264) of the study women. A total of 189 have agreed, 31 declined participation, 16 were deceased, 4 are in a nursing home, and 24 have yet to be contacted. Of the blood kits that have been mailed, 144 have already been returned. Isolation of DNA from peripheral blood for genetic analysis has been on-going as the samples get delivered to the Molecular Genetics Laboratory at the Mayo Clinic. Genotyping, analysis, and preparation of reports will not begin until all of the DNA samples have been collected. In summary, it is still early in the conduct of this research study but progress is being made according to the proposed timeline.

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FOREWORD

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Introduction

The radiographic appearance of the female breast depends on the relative proportions of fat, fibroglandular, and stromal tissue. Extensive research shows that women with greater proportions of fibroglandular and stromal tissue are at significantly increased risk of breast cancer than women with low proportions of dense tissue. We recently provided evidence that there appears to be a single major gene influence on mammographic breast density. The present project is an effort to confirm evidence for a major gene and localize it to one of the human chromosomes through genetic linkage analysis. Capitalizing on research data already collected on these families, we have identified a subset through simulation studies that would be informative for linkage analysis. From these women, we are obtaining blood samples as a source of DNA and generating anonymous DNA markers that span the human genome. These genetic markers would allow us to identify cosegregation of breast density trait with genetic markers as a first step to localize the gene.

Body

Considerable progress has been made on this project. As described in the Statement of Work, Task 1 was to select a subset of study families for analysis. This task has been completed. We have identified 57 families in which multiple members have previously obtained mammograms. Simulation studies were done on all 426 families to identify those that would provide the most information for genetic linkage analysis. Task 2 was to schedule the appointments for venipuncture. To date, letters of invitation (consent forms) have been sent to 264 women. A total of 189 have agreed, 31 declined participation, 16 were deceased, 4 are in a nursing home, and 24 have yet to be contacted. Of the blood kits that have been mailed, 144 have already been returned. Work on Task 2 will continue. Task 3 is to isolate DNA from peripheral blood for genetic analysis. This work has been ongoing as the samples have been delivered to the Molecular Genetics Laboratory at the Mayo Clinic. Tasks 4-6 (genotyping, analysis, and preparation of reports) will not begin until all of the DNA has been collected. In addition, we have been working on updating our original phenotype of percent breast density to a computer-assisted estimate of percent breast density that we will compare with our subjective determination initially proposed for this linkage analysis.

Key Research Accomplishments

There are no results generated from this study at this time

Reportable Outcomes

None.

Conclusions

We are still in the data collection phase. No conclusions will be possible until we have done genotyping and data analysis.

References

None.

Appendices

None.